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RAW SEQUENCE LISTING .

DATE: 02/07/2002

PATENT APPLICATION: US/10/051,852

TIME: 19:22:15

Input Set : N:\Crf3\RULE60\10051852.txt

Output Set: N:\CRF3\02072002\J051852.raw

SEQUENCE LISTING

C--> 3 (1) GENERAL INFORMATION:

(i) APPLICANT: Blackburn, Michael
 Church, William
 Gross, Mitchell
 Feuerstein, Giora
 Nichols, Andrew
 Padlan, Eduardo
 Patel, Arunbhai
 Sylvester, Daniel

(ii) TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
 OF THROMBOSIS

(iii) NUMBER OF SEQUENCES: 111

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: SmithKline Beecham Corporation
 (B) STREET: 709 Swedeland Road
 (C) CITY: King of Prussia
 (D) STATE: PA
 (E) COUNTRY: USA
 (F) ZIP: 19406

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
 (B) COMPUTER: IBM Compatible
 (C) OPERATING SYSTEM: DOS
 (D) SOFTWARE: FastSEQ Version 1.5

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US/10/051,852
 (B) FILING DATE: 17-Jan-2002
 (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 09/344,050
 (B) FILING DATE: 25-JUN-1999
 (A) APPLICATION NUMBER: 08/783,853
 (B) FILING DATE: 16-JAN-1997

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Baumeister, Kirk
 (B) REGISTRATION NUMBER: 33,833
 (C) REFERENCE/DOCKET NUMBER: P50438

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 610-270-5096
 (B) TELEFAX:
 (C) TELEX:

57 (2) INFORMATION FOR SEQ ID NO: 1:

ENTERED

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59      (i) SEQUENCE CHARACTERISTICS:
60          (A) LENGTH: 20 base pairs
61          (B) TYPE: nucleic acid
62          (C) STRANDEDNESS: single
63          (D) TOPOLOGY: linear
65      (ii) MOLECULE TYPE: cDNA
66      (iii) HYPOTHETICAL: NO
C--> 67      (iv) ANTI-SENSE: NO
W--> 68      (v) FRAGMENT TYPE:
69      (vi) ORIGINAL SOURCE:
71      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
73  CATCCTAGAG TCACCGAGGA                                20
75 (2) INFORMATION FOR SEQ ID NO: 2:
77      (i) SEQUENCE CHARACTERISTICS:
78          (A) LENGTH: 21 base pairs
79          (B) TYPE: nucleic acid
80          (C) STRANDEDNESS: single
81          (D) TOPOLOGY: linear
83      (ii) MOLECULE TYPE: cDNA
84      (iii) HYPOTHETICAL: NO
C--> 85      (iv) ANTI-SENSE: NO
W--> 86      (v) FRAGMENT TYPE:
87      (vi) ORIGINAL SOURCE:
89      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
91  AGCTGCCCAA AGTGCCCAAG C                                21
93 (2) INFORMATION FOR SEQ ID NO: 3:
95      (i) SEQUENCE CHARACTERISTICS:
96          (A) LENGTH: 36 base pairs
97          (B) TYPE: nucleic acid
98          (C) STRANDEDNESS: single
99          (D) TOPOLOGY: linear
101     (ii) MOLECULE TYPE: cDNA
102     (iii) HYPOTHETICAL: NO
C--> 103     (iv) ANTI-SENSE: NO
W--> 104     (v) FRAGMENT TYPE:
105     (vi) ORIGINAL SOURCE:
107     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
109  CTAACACTCA TTCCTGTTGA AGCTCTTGAC AATGGG                36
111 (2) INFORMATION FOR SEQ ID NO: 4:
113     (i) SEQUENCE CHARACTERISTICS:
114         (A) LENGTH: 21 base pairs
115         (B) TYPE: nucleic acid
116         (C) STRANDEDNESS: single
117         (D) TOPOLOGY: linear
119     (ii) MOLECULE TYPE: cDNA
120     (iii) HYPOTHETICAL: NO
C--> 121     (iv) ANTI-SENSE: NO
W--> 122     (v) FRAGMENT TYPE:
123     (vi) ORIGINAL SOURCE:

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125      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
127      GATTTTCARG TGCAGATTTT C                                21
129  (2) INFORMATION FOR SEQ ID NO: 5:
131      (i) SEQUENCE CHARACTERISTICS:
132          (A) LENGTH: 363 base pairs
133          (B) TYPE: nucleic acid
134          (C) STRANDEDNESS: single
135          (D) TOPOLOGY: linear
137      (ii) MOLECULE TYPE: cDNA
138      (iii) HYPOTHETICAL: NO
C--> 139      (iv) ANTI-SENSE: NO
W--> 140      (v) FRAGMENT TYPE:
141      (vi) ORIGINAL SOURCE:
143      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
145      CAGATCCAGT TGGTGCAGTC TGGACCTGAG CTGAAGAAGC CTGGAGAGAC AGTCAAGATC      60
146      TCCTGCAAGG CTTCTGGGTA CACCTTCACA AACTATGGAA TGAAC TGGGT GAAGCAGGCT      120
147      CCAGGAAAGG GTTTAAAGTG GATGGGCTGG ATAAACACCA GAAATGGAAA GTCAACATAT      180
148      GTTGATGACT TCAAGGGACG GTTGCCTTC TCTTTGAAA GCTCTGCCAG CACTGCCAAT      240
149      TTGCAGATCG ACAACCTCAA AGATGAGGAC ACGGCTACAT ATTTCTGTAC AAGAGAAGGG      300
150      AATATGGATG GTTACTTCCC TTTACTTAC TGGGGCCAAG GGA CTCTGGT CACTGTCTCT      360
151      GCA                                                                363
153  (2) INFORMATION FOR SEQ ID NO: 6:
155      (i) SEQUENCE CHARACTERISTICS:
156          (A) LENGTH: 321 base pairs
157          (B) TYPE: nucleic acid
158          (C) STRANDEDNESS: single
159          (D) TOPOLOGY: linear
161      (ii) MOLECULE TYPE: cDNA
162      (iii) HYPOTHETICAL: NO
C--> 163      (iv) ANTI-SENSE: NO
W--> 164      (v) FRAGMENT TYPE:
165      (vi) ORIGINAL SOURCE:
167      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
169      CAAATTGTTC TCTCCCAGTC TCCAGCAATC CTGTCTGCAT CTCCAGGGGA GAAGGTCACA      60
170      ATGACTTGCA GGGCCAGCTC AAGTGTAAT TACATGCACT GGTACCAGCA GAAGCCAGGA      120
171      TCCTCCCCCA AACCCCTGGAT TTATGCCACA TCCAACCTGG CTTCTGGAGT CCCTGCTCGC      180
172      TTCAGTGGCA GTGGGTCTGG GACCTCTTAC TCTCTCACA TCAGCAGAGT GGAGGCTGAA      240
173      GATGCTGCCA CTTATTACTG CCAGCAGTGG AGTATTAACC CACGGACGTT CGGTGGAGGC      300
174      ACCAAGCTGG AAATCAAACG G                                                                321
176  (2) INFORMATION FOR SEQ ID NO: 7:
178      (i) SEQUENCE CHARACTERISTICS:
179          (A) LENGTH: 121 amino acids
180          (B) TYPE: amino acid
181          (C) STRANDEDNESS: single
182          (D) TOPOLOGY: linear
184      (ii) MOLECULE TYPE: peptide
185      (iii) HYPOTHETICAL: NO
C--> 186      (iv) ANTI-SENSE: NO
187      (v) FRAGMENT TYPE: internal

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188      (vi) ORIGINAL SOURCE:
190      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
192  Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
193    1           5           10           15
194  Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
195           20           25           30
196  Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met
197           35           40           45
198  Gly Trp Ile Asn Thr Arg Asn Gly Lys Ser Thr Tyr Val Asp Asp Phe
199           50           55           60
200  Lys Gly Arg Phe Ala Phe Ser Leu Glu Ser Ser Ala Ser Thr Ala Asn
201           65           70           75           80
202  Leu Gln Ile Asp Asn Leu Lys Asp Glu Asp Thr Ala Thr Tyr Phe Cys
203           85           90           95
204  Thr Arg Glu Gly Asn Met Asp Gly Tyr Phe Pro Phe Thr Tyr Trp Gly
205           100          105          110
206  Gln Gly Thr Leu Val Thr Val Ser Ala
207           115          120
209 (2) INFORMATION FOR SEQ ID NO: 8:
211      (i) SEQUENCE CHARACTERISTICS:
212          (A) LENGTH: 5 amino acids
213          (B) TYPE: amino acid
214          (C) STRANDEDNESS: single
215          (D) TOPOLOGY: linear
217      (ii) MOLECULE TYPE: peptide
218      (iii) HYPOTHETICAL: NO
C--> 219      (iv) ANTI-SENSE: NO
220      (v) FRAGMENT TYPE: internal
221      (vi) ORIGINAL SOURCE:
223      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
225  Asn Tyr Gly Met Asn
226    1           5
228 (2) INFORMATION FOR SEQ ID NO: 9:
230      (i) SEQUENCE CHARACTERISTICS:
231          (A) LENGTH: 17 amino acids
232          (B) TYPE: amino acid
233          (C) STRANDEDNESS: single
234          (D) TOPOLOGY: linear
236      (ii) MOLECULE TYPE: peptide
237      (iii) HYPOTHETICAL: NO
C--> 238      (iv) ANTI-SENSE: NO
239      (v) FRAGMENT TYPE: internal
240      (vi) ORIGINAL SOURCE:
242      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
244  Trp Ile Asn Thr Arg Asn Gly Lys Ser Thr Tyr Val Asp Asp Phe Lys
245    1           5           10           15
246  Gly
249 (2) INFORMATION FOR SEQ ID NO: 10:
251      (i) SEQUENCE CHARACTERISTICS:

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252      (A) LENGTH: 12 amino acids
253      (B) TYPE: amino acid
254      (C) STRANDEDNESS: single
255      (D) TOPOLOGY: linear
257      (ii) MOLECULE TYPE: peptide
258      (iii) HYPOTHETICAL: NO
C--> 259      (iv) ANTI-SENSE: NO
260      (v) FRAGMENT TYPE: internal
261      (vi) ORIGINAL SOURCE:
263      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
265  Glu Gly Asn Met Asp Gly Tyr Phe Pro Phe Thr Tyr
266    1             5             10
268 (2) INFORMATION FOR SEQ ID NO: 11:
270      (i) SEQUENCE CHARACTERISTICS:
271          (A) LENGTH: 107 amino acids
272          (B) TYPE: amino acid
273          (C) STRANDEDNESS: single
274          (D) TOPOLOGY: linear
276      (ii) MOLECULE TYPE: peptide
277      (iii) HYPOTHETICAL: NO
C--> 278      (iv) ANTI-SENSE: NO
279      (v) FRAGMENT TYPE: internal
280      (vi) ORIGINAL SOURCE:
282      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
284  Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro Gly
285    1             5             10             15
286  Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Asn Tyr Met
287             20             25             30
288  His Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr
289             35             40             45
290  Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
291             50             55             60
292  Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Glu Ala Glu
293             65             70             75             80
294  Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ile Asn Pro Arg Thr
295             85             90             95
296  Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
297             100            105
299 (2) INFORMATION FOR SEQ ID NO: 12:
301      (i) SEQUENCE CHARACTERISTICS:
302          (A) LENGTH: 10 amino acids
303          (B) TYPE: amino acid
304          (C) STRANDEDNESS: single
305          (D) TOPOLOGY: linear
307      (ii) MOLECULE TYPE: peptide
308      (iii) HYPOTHETICAL: NO
C--> 309      (iv) ANTI-SENSE: NO
310      (v) FRAGMENT TYPE: internal
311      (vi) ORIGINAL SOURCE:

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VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10051852.txt

Output Set: N:\CRF3\02072002\J051852.raw

L:3 M:220 C: Keyword misspelled or invalid format, [(1) GENERAL INFORMATION:]
L:34 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:35 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:67 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:68 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=1
L:85 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:86 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=2
L:103 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:104 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=3
L:121 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:122 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=4
L:139 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:140 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=5
L:163 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:164 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=6
L:186 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:219 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:238 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:259 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:278 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:309 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:328 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:347 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:366 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:367 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=15
L:385 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:386 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=16
L:404 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:405 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=17
L:423 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:424 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=18
L:442 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:443 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=19
L:493 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:524 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:525 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=21
L:542 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:543 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=22
L:560 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:561 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=23
L:591 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:612 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:613 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=25
L:631 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:632 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=26
L:649 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:650 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=27
L:667 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]

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L:668 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=28
L:686 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:687 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=29
L:705 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:706 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=30
L:759 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:792 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:793 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=32
L:812 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:813 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=33
L:832 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:833 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=34
L:878 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:907 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:908 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=36
L:925 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:926 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=37
L:943 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:944 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=38
L:973 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:994 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:995 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=40
L:1012 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1013 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=41
L:1030 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1031 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=42
L:1048 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1049 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=43
L:1098 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1129 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1130 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=45
L:1149 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1150 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=46
L:1169 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1170 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=47
L:1239 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=49
L:1257 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=50
L:1275 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=51
L:1362 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=53
L:1381 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=54
L:1421 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=56
L:1502 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=58
L:1520 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=59
L:1557 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=61
L:1638 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=63
L:1658 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=64
L:1678 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=65
L:1753 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=67
L:1771 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=68

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L:1789 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=69
L:1827 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=71
L:1845 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=72